In the Specification:

Please insert the enclosed Sequence Listing immediately after the section of the specification entitled "Abstract of the Invention" on page 40.

In the Claims:

Please cancel claims 1-29 and add the following claims:

30. A method of screening for a compound that interferes with the association of a human Bad interacting polypeptide with human Bad, said human Bad comprising an isolated human Bad polypeptide encoded by a nucleic acid molecule comprising the nucleotide sequence shown in SEQ ID NO:1 or a nucleotide sequence that has greater than 85% nucleotide identify to the nucleotide sequence shown in SEQ ID NO:1 wherein said screening comprises contacting human Bad, or a human Bad derived fragment which retains the ability to interact with a human Bad interacting polypeptide, in the presence of an interacting polypeptide with a sample suspected of containing a compound capable of interfering with the human Bad polypeptide association and determining the interaction between human Bad and human Bad interacting polypeptide thereby screening for a compound which interferes with the association of a human Bad interacting polypeptide with human Bad.

31. The method of claim 30, wherein said interaction is a binding interaction.

32. The method of claim 30, wherein said human Bad interacting polypeptide comprises Bcl-X_L.

33. The method of claim 30, wherein said human Bad interacting polypeptide comprises Bcl-2.

34. The method of claim 30, wherein said Bad fragment is a Bcl-X_L binding domain.

35. The method of claim 30, wherein said Bad fragment comprises a fragment of no greater than 95 contiguous amino acids of the 3' end of SEQ ID NO:2, wherein the fragment binds Bcl-X_L or Bcl-2 and wherein the fragment contains at least one amino acid that differs when aligned with SEQ ID NO:3.

36. The method of claim 31, wherein said binding is determined by the detection of a reporter gene.

37. The method of claim 31, wherein said binding is determined by an enzyme linked immunosorbant assay (ELISA).